

Fig 1.

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SEQID22      MLLLGAVLLLLLALPGHDQETTTQGPVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG  60
SEQID23      -----
SEQID24      MLLLGAVLLLLLALPGHDQETTTQGPVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG  60
SEQID25      MLLLGAVLLLLLALPGHDQETTTQGPVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG  60

SEQID22      TPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFVSGLE 120
SEQID23      -----MPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFVSGLE  36
SEQID24      TPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEA----- 108
SEQID25      TPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFVSGLE 120

SEQID22      TYVTIPNMPIRFTKIFYNQNHYDGSTGKFHCNIPGLYFAYHITVYMKDVKVSLFKKDK 180
SEQID23      TYVTIPNMPIRFTKIFYNQNHYDGSTGKFHCNIPGLYFAYHITVYMKDVKVSLFKKDK  96
SEQID24      ----- 108
SEQID25      TYVTIPNMPIRFTKIFYNQNHYDGSTGKFHCNIPGLY----- 158

SEQID22      AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF 237
SEQID23      AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF 153
SEQID24      -----LLS-PTCPFALPRSSTISKTTMMAP--LVNSTATFLGC 143
SEQID25      ----- 158

SEQID22      LLYHDTN----- 244
SEQID23      LLYHDTN----- 160
SEQID24      T----T-LP-TTSQSI- 153
SEQID25      -----LHRLSSLP 166

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Fig 2.

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SEQID28      MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG  60
SEQID30      MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPGH-----  52
SEQID29      MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG  60
SEQID26      MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG  60
SEQID27      -----

SEQID28      ---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAA-----AASL  113
SEQID30      -----  52
SEQID29      ---TPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAA-----  110
SEQID26      RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAVYRSAFSV  120
SEQID27      -----MTGAEGPRGFPGTPGRKGEPGEAAVYRSAFSV  33

SEQID28      -----  109
SEQID30      -----  52
SEQID29      -----  110
SEQID26      GLETRVTVPNVPIRFTKIFYNQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFK  180
SEQID27      GLETRVTVPNVPIRFTKIFYNQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFK  93

SEQID28      -----FPMYP  118
SEQID30      -----IKIK-----FEGHP-----PG-----  63
SEQID29      -----VYRSAFSVGLETRVTV  129
SEQID26      KDKAVLFTYDQYQEKNVDAQ-----SGSVLLHLEVGDQVWLQ-----  217
SEQID27      KDKAVLFTYDQYQEKNVDAQ-----SGSVLLHLEVGDQVWLQ-----  130

SEQID28      FALLRSSTTNRIIMTAALASSTATFRDSTTSLTTSRCT---  156
SEQID30      --RLNCAKIWHFLQD-----  76
SEQID29      NVPIRFTKIFYNQNH-HYDGSTGKFYCNIPGLYYIWLSSLP  169
SEQID26      --VYGDGDHNGLYADNVNDSTFTGFLLYHDTN-----  247
SEQID27      --VYGDGDHNGLYADNVNDSTFTGFLLYHDTN-----  160

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Fig 3.

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SEQID31      MPSPGTVCSELLLGLWLDLDMAGSSFLSPEHQRVQQRKESKKP----- 44
SEQID32      MPSPGTVCSELLLGLWLDLDMAGSSFLSPEHQRVQVRPPHKAP-----HV 47

SEQID31      PAKLQPRALAGWLRPEDGGQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQD 104
SEQID32      PALPLSNQLCDLEQQRHWASVFSQSTKDCSDLTVSGRTWGLRV----- 91

SEQID31      ILWEEAKEAPADK----- 117
SEQID32      LNRLFPSSRRERSRRSHQFSCSPEL 116
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Fig 4.

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SEQID33      MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH 60
SEQID38      -----MLQGKKVIVTGASKGIGREMAHYHLAKMGAH 30
SEQID36      MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH 60
SEQID35      MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH 60
SEQID37      MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH 60
SEQID39      MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH 60
SEQID34      MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH 60

SEQID33      VVVTARSKETLQKVSSHCLLGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 120
SEQID38      VVVTARSKETLQKVSSHCLLGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 90
SEQID36      VVVTARSKETLQKVSSHCLLGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 120
SEQID35      VVVTARSKETLQKVSSHCLLGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 120
SEQID37      VVVTASS-----AHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 102
SEQID39      VVVTARSKETLQKVSSHCLLGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 120
SEQID34      VVVTASS-----AHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH 102

SEQID33      ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV 180
SEQID38      ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV 150
SEQID36      ITNTSLNLFHDDIHHVR-----PMLKQSNGSIVVVSSLAGKVAYPMV 162
SEQID35      ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV 180
SEQID37      ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLAGKVAYPMV 162
SEQID39      ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNGSIVVVSSLA----- 172
SEQID34      ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNGSMCAL----- 150

SEQID33      AAYSASKFALDGGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 240
SEQID38      AAYSASKFALDGGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 210
SEQID36      AAYSASKFALDGGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 222
SEQID35      AAYSASKFALDGGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 240
SEQID37      AAYSASKFALDGGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEE 222
SEQID39      -----ETAMKAVSGIVHMQAAPKEE 192
SEQID34      -----LLECYHVHVLSSX---- 163

SEQID33      CALEIIKGGALRQEEVYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 292
SEQID38      CALEIIKGGALRQEEVYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 262
SEQID36      CALEIIKGGALRQEEVYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 274
SEQID35      CALEIIKGGALRQEEVYDSSLWTTLLIRNPCRKILEFLYSTSYNMEGLFCLMFI 295
SEQID37      CALEIIKGGALRQEEVYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 274
SEQID39      CALEIIKGGALRQEEVYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK--- 244
SEQID34      -----

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Fig 5.

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SEQID40      MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAHLSKMGH 60
SEQID41      MAVMKNYLLPILVLFLAY----- 18
SEQID42      MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAHLSKMGH 60

SEQID40      VVLTARSEEGQLQVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGDLMLILNH 120
SEQID41      YYYSTNEEFRLQKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGDLMLILNH 78
SEQID42      VVLTARSEEGQLQVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGDLMLILNH 120

SEQID40      ITQTSLSLFDHDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNCSIIVISSLAGKMTQPMI 180
SEQID41      ITQTSLSLFDHDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNCSIIVISSLAGKMTQPMI 138
SEQID42      ITQTSLSLFDHDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNCSIIVISSLAGGRTVPQQ 180

SEQID40      APYSASKFALDGGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE 240
SEQID41      APYSASKFALDGGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE 198
SEQID42      RSRSVTPDSRGP----- 192

SEQID40      CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN 292
SEQID41      CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN 250
SEQID42      -----

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Fig 6.

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SEQID1      CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTCTACTGCTATTAG
SEQID2      -----
SEQID3      -----
SEQID4      -----

SEQID1      CTCTGCCCCGGGCATGACCAGGAAACCACGACTCAAGGGCCCCGGAGTCCTGCTTCCCCTGC
SEQID2      -----
SEQID3      -----
SEQID4      -----

SEQID1      CCAAGGGGGCCTGCACAGGTTGGATGGCGGGCATCCCAGGGCATCCGGGCCATAATGGGG
SEQID2      -----
SEQID3      -----
SEQID4      -----

SEQID1      CCCCAGGCCGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGATCCAG
SEQID2      -----ATG-----
SEQID3      -----CTGATTCCAT-----
SEQID4      -----CTGATTCCAT-----
                      **

SEQID1      GTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACCCG--GGGCTGAAGGTCC
SEQID2      -----ACCCG--GGGCTGAAGGTCC
SEQID3      -----ACCAGAGGGGCTCAGGATGC
SEQID4      -----ACCAGAGGGGCTCAGGATGC
                      *** * ***** * * * *

SEQID1      -----CCGAG-GCT-TTC--CGGG-AAT-----CCAAGGCAGGAA-AGGAGAACCTGG
SEQID2      -----CCGAG-GCT-TTC--CGGG-AAT-----CCAAGGCAGGAA-AGGAGAACCTGG
SEQID3      TGTGTCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCCGGGCATGACCAGGA-AACCACG
SEQID4      TGTGTCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCCGGGCATGACCAGGA-AACCACG
                      * * * * * * * * * * * * * * * * * * * * * * * * * *

SEQID1      A--GAAGGTGCCTATGTA----TACCGCT---CA----GCATTCAAGT-TGGGATTGGA
SEQID2      A--GAAGGTGCCTATGTA----TACCGCT---CA----GCATTCAAGT-TGGGATTGGA
SEQID3      ACTCAAGGGCCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTGGATGGCG
SEQID4      ACTCAAGGGCCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTGGATGGCG
                      * * * * * * * * * * * * * * * * * * * * * * * * * *

SEQID1      GACTTACGTTACTATCC---CCAACATG---CCCATTGCT--TTACCAAGAT-----
SEQID2      GACTTACGTTACTATCC---CCAACATG---CCCATTGCT--TTACCAAGAT-----
SEQID3      GGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
SEQID4      GGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
                      * * * * * * * * * * * * * * * * * * * * * * * * * *

SEQID1      -CTTCT-ACAA--TCAGCAA---AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID2      -CTTCT-ACAA--TCAGCAA---AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID3      CCTGGTGAGAAGGTTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGT
SEQID4      CCTGGTGAGAAGGTTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGT
                      * * * * * * * * * * * * * * * * * * * * * * * * * *

SEQID1      GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID2      GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID3      GAAACCGGAGTACCCGGGGCTGAAGTCCCCGAGGCTTCCGGG---AATCCA-AGGCA
SEQID4      GAAACCGGAGTACCCGGGGCTGAAGTCCCCGAGGCTTCCGGG---AATCCA-AGGCA
                      * * * * * * * * * * * * * * * * * * * * * * * * * *

SEQID1      GGATGTGAAGGTACGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID2      GGATGTGAAGGTACGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID3      GGA----AAGGAGAACCT-----GGAGAAGG---TGC-----
SEQID4      GGA----AAGGAGAACCT-----GGAGAAGG---TGCCTATGTATACCGCTCAGCA
                      *** * * * * * * * * * * * * * * * * *

SEQID1      GTACCAGGAAATAATGTGGACC--AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT

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SEQID2 GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT
 SEQID3 -----GTTACTATCC-CCAACATGCCCATTC
 SEQID4 TT--CAG-----TGTGGGATTGGAGACTTACGTTACTATCC-CCAACATGCCCATTC
 * * * * *

SEQID1 GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
 SEQID2 GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
 SEQID3 GCTTTACCAAGATCTT-CTACA-----ATCAGCAAAACCACTATGATGG-CTCCA--CTG
 SEQID4 GCTTTACCAAGATCTT-CTACA-----ATCAGCAAAACCACTATGATGG-CTCCA--CTG
 * * * * *

SEQID1 ATAA-TGACAATG---ACTCC-----AC-----
 SEQID2 ATAA-TGACAATG---ACTCC-----AC-----
 SEQID3 GTAAATTCCACTGCAACATTCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATA
 SEQID4 GTAAATTCCACTGCAACATTCTGGGCTGTAC-----
 * * * * *

SEQID1 -----
 SEQID2 -----
 SEQID3 TGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATC
 SEQID4 -----

SEQID1 -----
 SEQID2 -----
 SEQID3 AGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGG
 SEQID4 -----

SEQID1 -----
 SEQID2 -----
 SEQID3 GCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATA
 SEQID4 -----

SEQID1 -----CTTCACAGGCTTTCTTCTTCTACCATGACACCAACTGATCACCAC
 SEQID2 -----CTTCACAGGCTTTCTTCTTCTACCATGACACCAACTGA-----
 SEQID3 ATGACAATGACTCCACCTTCACAGGCTTTCTTCTTCTACCATGACACCAACTGA-----
 SEQID4 -----CTTCACAGGCTTTCTTCTTCTACCATGACACCAACTGA-----
 * * * * *

SEQID1 TAACTCAGAGCCTCCTCCAGGCCAAACAGCCCCAAAGTCAATTAAAGGCTTTCAGTACGG
 SEQID2 -----
 SEQID3 -----
 SEQID4 -----

SEQID1 TTAGGAAGTTGATTATTATTTAGTTGGAGGCCTTTAGATATTATTCATTCATTTACTCAT
 SEQID2 -----
 SEQID3 -----
 SEQID4 -----

Fig 7.

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SEQID5      ATGAGACCTGGCCACTTTCTCCTCATTCTGTCTGTACGATTGTCAGTGGATCTGACGAC 60
SEQID6      -----GCTCATTTCATCTTTTAATTCA----- 21
SEQID7      ATGAGACCTGGCCACTTTCTCCTCATTCTGTCTGTACGATTGTCAGTGGATCTGACGAC 60
SEQID8      -----
SEQID9      -----

SEQID5      ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCAG 120
SEQID6      CCCATAAAGGCTTTGAAACTAAGGCTGGAGATGAACCTTAT-----AGGAGCCTGCCAGG 76
SEQID7      ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCAG 120
SEQID8      -----
SEQID9      -----

SEQID5      TCATGCCGAAGATGACGTTACTACAACCTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC 180
SEQID6      CCGTG--GAGAGTGAGGAAGCAGAGATGACGGAGATGATGCTTTCTTGTCTGTGA-- 132
SEQID7      TCATGCCGAAGATGACGTTACTACAACCTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC 180
SEQID8      -----
SEQID9      -----

SEQID5      CAAGGGAACCTTGTGCAGGTTGGATGGCAGGCATCCAGGACATCCTGGCCACAATGGCAC 240
SEQID6      -AATGGATTGTGGGTAGA---GGTCCGGAGATAATGCCTCTTGTCTGGAAACAGT----- 183
SEQID7      CAAGGGAACCTTGTGCAGGTTGGATGGCAGGCATCCAGGACATCCTGGCCACAATGGCAC 240
SEQID8      -----
SEQID9      -----

SEQID5      ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG 300
SEQID6      -CTGGGCAGTTCTGT---CCCGCCATTC---ACAGAATTCCTCTCACTT---TCTAGG 232
SEQID7      ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG 300
SEQID8      -----
SEQID9      -----

SEQID5      TCTTCTTGGTCTTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG 360
SEQID6      TCTTCTTGGTCTTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG 292
SEQID7      TCTTCTTGGTCTTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG 360
SEQID8      -----
SEQID9      -----

SEQID5      GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG 420
SEQID6      GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG 352
SEQID7      GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGC----- 408
SEQID8      -----
SEQID9      -----

SEQID5      CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTTCGCTT 480
SEQID6      CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTTCGCTT 412
SEQID7      -----GTCAGTGTCCCAATGTACCCATTTCGCTT 437
SEQID8      -----ATGAGACC--TGGCCACTTTCTCCT 23
SEQID9      -----ATGAGACC--TGGCCACTTTCTCCT 23
                      **  **  **  *  *  *  *  *

SEQID5      TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG 540
SEQID6      TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG 472
SEQID7      TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG 497
SEQID8      CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG 79
SEQID9      CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG 79
                      *  *      ***  ***  *      ***  *  *  *  *  *  *  *  *

SEQID5      CAACATTCGGGGACTCTACTACTTCTCTTACCACATCACGGTGATACATGAAAGATGTGAA 600
SEQID6      CAACATTCGGGGACTCTACTACTTCTCTTACCACATCACGGTGATACATGAAAGATGTGAA 532
SEQID7      CAACATTCGGGGACTCTACTACTTCTCTTACCACATCACGGTGATACATGAAAGATGTGAA 557
SEQID8      CTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCAGT---CATGCCGAAGATGAC 136
SEQID9      CTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCAGT---CATGCCGAAGATGAC 136

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* * * * *      * * * * *      * * * * *      * * * * *      * * * * *
SEQID5      GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 660
SEQID6      GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 592
SEQID7      GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAA 617
SEQID8      GTTACTACAAC---GAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCA---AGGGAAC 189
SEQID9      GTTACTACAAC---GAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCA---AGGGAAC 189
* * * * *      * * * * *      * * * * *      * * * * *      * * * * *

SEQID5      GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 720
SEQID6      GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 652
SEQID7      GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG 677
SEQID8      TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC---CTGGCCACAATG---GCACACC 243
SEQID9      TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC---CTGGCCACATAA---AAATATA 243
* * * * *      * * * * *      * * * * *      * * * * *      * * * * *

SEQID5      GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 780
SEQID6      GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 712
SEQID7      GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC 737
SEQID8      AGGCCGTGTATGGCAGAGA-TGGCAGCTCCTGGA---GAGAAGGGAGAGAAAGGA-GATGC 297
SEQID9      ATTC-----GAGG-GGCATCCACCAGG---CCGGCTGAATTGTGCCAA-AATAT 287
* * * * *      * * * * *      * * * * *      * * * * *      * * * * *

SEQID5      TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCCA 840
SEQID6      TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCCA 772
SEQID7      TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCCA 797
SEQID8      AGGTCTTCTTGGTCTTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCC 357
SEQID9      GGCACCTTCCTG-----CAAGATAA----- 306
* * * * *      * * * * *      * * * * *      * * * * *      * * * * *

SEQID5      TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 900
SEQID6      TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 832
SEQID7      TACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTT 857
SEQID8      ACGGGGCTTCCCCGGAACCCCTGGCAGGAAGGAGAGCCTGGAGAAGCCGCTTATGTGTA 417
SEQID9      -----

SEQID5      TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTIONTCTGTTTCAATAAAC 960
SEQID6      TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTIONTCTGTTTCAATAAAC 892
SEQID7      TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTIONTCTGTTTCAATAAAC 917
SEQID8      TCGCTCAGCGTTCAGTGTGGGCTGGAGACCCGCTCACTGTTCCCAATGTACCCATTTCG 477
SEQID9      -----

SEQID5      GACTTTATAAAAAATAATTTGTGTTCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCA 1020
SEQID6      GACTTTATAAAAAATAATTTGTGTTCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCA 952
SEQID7      GACTTTATAAAAAATAATTTGTGTTCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCA 977
SEQID8      CTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTA 537
SEQID9      -----

SEQID5      CGACTCTTACATGGTAGCAATAACAGAATGAAATCACATTTGGTATGGGGGCTTCACAA 1080
SEQID6      CGACTCTTACATGGTAGCAATAACAGAATGAAATCACATTTGGTATGGGGGCTTCACAA 1012
SEQID7      CGACTCTTACATGGTAGCAATAACAGAATGAAATCACATTTGGTATGGGGGCTTCACAA 1037
SEQID8      CTGCAACATTCCGGGACTCTACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGAC 597
SEQID9      -----

SEQID5      TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTCTGCTCACTGTACACAAATAT 1140
SEQID6      TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTCTGCTCACTGTACACAAATAT 1072
SEQID7      TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTCTGCTCACTGTACACAAATAT 1097
SEQID8      TGCAACTACCCATAGCCCATACACAGGAGAATCATGGAACAGTCGACACACTTTCAGCT 657
SEQID9      -----

SEQID5      TGTTACATAAAACCTATAATGTAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1200
SEQID6      TGTTACATAAAACCTATAATGTAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1132
SEQID7      TGTTACATAAAACCTATAATGTAATATGAAATACAGTGATTACTCTTCTCACAGGCTG 1157
SEQID8      TAGTTTGAGAGATTGATTTTATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTG 717
SEQID9      -----

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SEQID5      ASTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGGAAAAAAA 1260
SEQID6      AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG----- 1184
SEQID7      AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG----- 1209
SEQID8      ACTCACTTGTTCATTAAACGACTTTATAAAAAATAATTTGTGTTCTAGTCCAGAAAAAA 777
SEQID9      -----

```

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SEQID5      AAAAAAAAAAAGAAAACTTTAGAGCACACTGGCGGCCGTTACTAG----- 1306
SEQID6      -----
SEQID7      -----
SEQID8      AGGCACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAAATCACATT 837
SEQID9      -----

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SEQID5      -----
SEQID6      -----
SEQID7      -----
SEQID8      TGGTATGGGGCTTCACAATATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTCT 897
SEQID9      -----

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SEQID5      -----
SEQID6      -----
SEQID7      -----
SEQID8      GCTCACTGTACACAAATATTGTTACATAAACCCCTATAATGTAAATATGAAATACAGTGA 957
SEQID9      -----

```

```

SEQID5      -----
SEQID6      -----
SEQID7      -----
SEQID8      TTACTCTTCTCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAG 1017
SEQID9      -----

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SEQID5      -----
SEQID6      -----
SEQID7      -----
SEQID8      GGATAAATTGG 1028
SEQID9      -----

```

Fig 8.

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SEQID10      ACTCTGGATGGGTGCTGTTTAGACAAACGCCGCTCCTATATAAGACCTGACAGCACAGG 60
SEQID11      ACTCTGGATGGGTGCTGTTTAGACAAACGCCGCTCCTATATAAGACCTGACAGCACAGG 60
*****

SEQID10      CACCACTCCGCCAGGACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC 120
SEQID11      CACCACTCCGCCAGGACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC 120
*****

SEQID10      CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 180
SEQID11      CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA 180
*****

SEQID10      GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAG 240
SEQID11      GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--GTGAGACCTCCCCACAAAG 238
***** * * * *

SEQID10      CCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGT 300
SEQID11      CCCACATGTTGTTCAGCCCTGCCACTTAGCAA--CCAGCTCTGT-----GACCT 287
* * * * *

SEQID10      CAAGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGA 360
SEQID11      GGAGCAGCAGCGCCATCTC-TGGGCTTCA-GTCTTCTCCAGAGCACAAAGGACTCTGGG 345
***** * * * *

SEQID10      ATCAAGCTGTCAGGGGTTCACTACCAGCAGCACAGCC--AGGCCCTGGGGAAGTTTCTTC 418
SEQID11      TCTGACCT--CACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTTC 403
* * * * *

SEQID10      AGGACATCCTCTGGGAAGAG-GCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCAAGC 477
SEQID11      CCCCTTCCAGCAGAGAAAGGAGTCGAAGAAGCC--ACCAGCCAAGCTGCAGCCC-CGAGC 460
* * * * *

SEQID10      CTTACTCACCTCTCTCTAAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGC 537
SEQID11      TCTAGCAGGCTGGCTCC--GCCCGGAAGA-----TGGA-----GGTCAAGCAGA 502
* * * * *

SEQID10      AACTCCCACGACTGTTGTACAAGCTCAGGAGGCGAATAAATGTTCAAAGTGTATGCTGAT 597
SEQID11      AGGGGCAGAGGATGAACTGGAAGTCCGGG---TCGGTACCTCTGCAG-TTTTATGCTTCT 558
* * * * *

SEQID10      GTTCCAAATGGGAATTTATTTCAAAGAGGAAAAGTTAATATTTTACTTTAAAAAAATCAA 657
SEQID11      GTGGCAGCGAGGAGGGTGGG----- 579
* * * * *

SEQID10      AATAATAC 665
SEQID11      -----

```

Fig 9.

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SEQID15 -----
SEQID17 GGTGAAAAGGGAAAACCTGCCCAAATCCAGTTTTTGTTCAGTAACTTCCTTTGAGACAA 60
SEQID16 -----
SEQID12 -----
SEQID14 -----
SEQID18 -----
SEQID13 -----

SEQID15 -----
SEQID17 AGTCAGGAATCTGAGAGTAAGCACCTGCTAAGGGTGGGACAGGGGCTCTGTCTGGTATGC 120
SEQID16 -----
SEQID12 -----
SEQID14 -----
SEQID18 -----
SEQID13 -----

SEQID15 -----
SEQID17 CTCTCCCATGTTAAGAGCTAACAATAGTAATGGATAAGTCTCCAGGGCAACCAGGACCAC 180
SEQID16 -----
SEQID12 -----
SEQID14 -----
SEQID18 -----
SEQID13 -----

SEQID15 -----
SEQID17 TTCCAAGCATTCCTGTCTTGGGCTGCCTCGAGGGCTCCTCTGTCTTTGGGGAGTACTGA 240
SEQID16 -----
SEQID12 -----
SEQID14 -----
SEQID18 -----
SEQID13 -----

SEQID15 -----
SEQID17 TTGATGCCTGATGCCCAGAACTGGCCCACTCTGGCTTCTCTTTGGAGCTGTCTCTGCAGG 300
SEQID16 -----
SEQID12 -----
SEQID14 -----
SEQID18 -----
SEQID13 -----

SEQID15 -----GCA 3
SEQID17 CGCCTTCTGGCTGCCAGCTCGGTCTAGCATAGGGGACTTCTTCTTGGCCTGGGTTTCA 360
SEQID16 -----GCA 3
SEQID12 -----GCA 3
SEQID14 -----GCA 3
SEQID18 -----GCA 3
SEQID13 -----GCA 3
**

SEQID15 CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGTGTC 61
SEQID17 CCTTCTTGTATCAGGTGGCAGACCAGCTGGTTTCAG---TCCCAAATCAG-GTCTTCTGA 416
SEQID16 CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGTGTC 61
SEQID12 CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGTGTC 61
SEQID14 CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGTGTC 61
SEQID18 CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGTGTC 61
SEQID13 CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGTGTC 61
*  **  *  *  ***  *  *  **  *  *  **  ***  *****  *  *  **

SEQID15 CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID17 CTCCTCCAGAAACCAACCAACTTCTGAGCAGGAAATC-CTGCCCTCCCCAAAGAGTGG 475
SEQID16 CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119
SEQID12 CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCCTACAGGAGTCT 119

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SEQID14 CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTGTGTGTCTACAGGAGTCT 119
 SEQID18 CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTGTGTGTCTACAGGAGTCT 119
 SEQID13 CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTGTGTGTCTACAGGAGTCT 119
 * * * * *

SEQID15 TCAG--GCCAGCTCCCTGTGCGATGGCTTTTATGAAAAATATCTCCTCCCCATTCTGGG 177
 SEQID17 GAAACCGCAAAGGAAGAGAGATGAAACAGAAGGAAAGGCAGAGGAGGAGGAGAGAGA 535
 SEQID16 TCAG--GCCAGCTCCCTGTGCGATGGCTTTTATGAAAAATATCTCCTCCCCATTCTGGG 177
 SEQID12 TCAG--GCCAGCTCCCTGTGCGATGGCTTTTATGAAAAATATCTCCTCCCCATTCTGGG 177
 SEQID14 TCAG--GCCAGCTCCCTGTGCGATGGCTTTTATGAAAAATATCTCCTCCCCATTCTGGG 177
 SEQID18 TCAG--GCCAGCTCCCTGTGCGATGGCTTTTATGAAAAATATCTCCTCCCCATTCTGGG 177
 SEQID13 TCAG--GCCAGCTCCCTGTGCGATGGCTTTTATGAAAAATATCTCCTCCCCATTCTGGG 177
 * * * * *

SEQID15 GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCTAGACC----- 225
 SEQID17 GAGAAGAGAAAGAAAGAAAGAAACATCAATAAAAGAGTCTAGATTGTTTCGAAATC 595
 SEQID16 GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCTAGACC----- 225
 SEQID12 GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCTAGACC----- 225
 SEQID14 GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCTAGACC----- 225
 SEQID18 GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCTAGACC----- 225
 SEQID13 GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCTAGACC----- 225
 * * * * *

SEQID15 ---AGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 282
 SEQID17 TTGAGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 655
 SEQID16 ---AGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 282
 SEQID12 ---AGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 282
 SEQID14 ---AGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 282
 SEQID18 ---AGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 282
 SEQID13 ---AGAGATGCTCCAAGGAAAGAAAGTATTGTCTACAGGGGCCAGCAAAGGGATCGGAAG 282
 * * * * *

SEQID15 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 342
 SEQID17 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 715
 SEQID16 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 336
 SEQID12 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 342
 SEQID14 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 342
 SEQID18 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 342
 SEQID13 AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAA 336
 * * * * *

SEQID15 AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
 SEQID17 AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 775
 SEQID16 -----CTCAGCACACTA 348
 SEQID12 AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
 SEQID14 AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
 SEQID18 AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA 402
 SEQID13 -----CTCAGCACACTA 348
 * * * * *

SEQID15 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
 SEQID17 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 835
 SEQID16 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 408
 SEQID12 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
 SEQID14 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
 SEQID18 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 462
 SEQID13 CATTGCTGGCACCATTGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA 408
 * * * * *

SEQID15 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 522
 SEQID17 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 895
 SEQID16 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 468
 SEQID12 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 522
 SEQID14 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 522
 SEQID18 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 522
 SEQID13 GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCACACTTCTTTGAATCT 468
 * * * * *

SEQID15 TTTTCATGATGATATTACCATGTGCGC----- 550
 SEQID17 TTTTCATGATGATATTACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 955
 SEQID16 TTTTCATGATGATATTACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 528

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SEQID12      TTTTCATGATGATATTACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID14      TTTTCATGATGATATTACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID18      TTTTCATGATGATATTACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 582
SEQID13      TTTTCATGATGATATTACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT 528
                *****

SEQID15      -----CCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
SEQID17      GGTCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 1015
SEQID16      GGTCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 588
SEQID12      GGTCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID14      GGTCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID18      GGTCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT 642
SEQID13      GGTCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCAT-----GT 581
                *****

SEQID15      CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 647
SEQID17      CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 1074
SEQID16      CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 647
SEQID12      CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 701
SEQID14      CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT 701
SEQID18      CTCCTCTCTGGCTG----- 656
SEQID13      GCGCTCTTCTGCTGAA-----TGCTATCATGTTGTGCATCTGAGC 622
                ****

SEQID15      TTGCTTTGGATGGGTTCTTCTCTCCATCAGAAAGGAATATTCAAGTGTCCAGGGTCAATG 707
SEQID17      TTGCTTTGGATGGGTTCTTCTCTCCATCAGAAAGGAATATTCAAGTGTCCAGGGTCAATG 1134
SEQID16      TTGCTTTGGATGGGTTCTTCTCTCCATCAGAAAGGAATATTCAAGTGTCCAGGGTCAATG 707
SEQID12      TTGCTTTGGATGGGTTCTTCTCTCCATCAGAAAGGAATATTCAAGTGTCCAGGGTCAATG 761
SEQID14      TTGCTTTGGATGGGTTCTTCTCTCCATCAGAAAGGAATATTCAAGTGTCCAGGGTCAATG 761
SEQID18      -----
SEQID13      A-GTNGTTGATGG-----TCTCTCTCAT---AGAAGATATCAGG---CAGGCATGATA 668

SEQID15      TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 766
SEQID17      TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 1193
SEQID16      TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 766
SEQID12      TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 820
SEQID14      TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT 820
SEQID18      -----AAACAGCCATG-AAGGCAGTT 676
SEQID13      TACT-----TTGGTCTGCTATACCAGACGCTAGGCGTCTGATGCA--- 708
                *****

SEQID15      TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
SEQID17      TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 1253
SEQID16      TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 826
SEQID12      TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
SEQID14      TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 880
SEQID18      TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAAA 736
SEQID13      -----

SEQID15      GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 886
SEQID17      GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 1313
SEQID16      GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 886
SEQID12      GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 940
SEQID14      GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 940
SEQID18      GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG 796
SEQID13      -----

SEQID15      ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTTACTCAACGAGCTATAATATGGAC 946
SEQID17      ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTTACTCAACGAGCTATAATATGGAC 1373
SEQID16      ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTTACTCAACGAGCTATAATATGGAC 946
SEQID12      ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTTACTCAACGAGCTATAATATGGAC 1000
SEQID14      ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTTACTCAACGAGCTATAATATGGA- 999
SEQID18      ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTTACTCAACGAGCTATAATATGGAC 856
SEQID13      -----

SEQID15      AGATTCAATAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1006
SEQID17      AGATTCAATAACAAGTAGGAACCTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1433

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SEQID16      AGATTCTATAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1006
SEQID12      AGATTCTATAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 1060
SEQID14      -----GGGACTG 1006
SEQID18      AGATTCTATAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG 916
SEQID13      -----

SEQID15      TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCTCCAG 1066
SEQID17      TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCTCCAG 1493
SEQID16      TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCTCCAG 1066
SEQID12      TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCTCCAG 1120
SEQID14      TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCTCCAG 1066
SEQID18      TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCTCCAG 976
SEQID13      -----

SEQID15      AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCTCTAACATTTGCAAA 1126
SEQID17      AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCTCTAACATTTGCAAA 1553
SEQID16      AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCTCTAACATTTGCAAA 1126
SEQID12      AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCTCTAACATTTGCAAA 1180
SEQID14      AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCTCTAACATTTGCAAA 1126
SEQID18      AGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCTCTAACATTTGCAAA 1036
SEQID13      -----

SEQID15      ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
SEQID17      ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1613
SEQID16      ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
SEQID12      ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1240
SEQID14      ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1186
SEQID18      ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT 1096
SEQID13      -----

SEQID15      AGTAAACATAGGTATAAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
SEQID17      AGTAAACATAGGTATAAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1673
SEQID16      AGTAAACATAGGTATAAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
SEQID12      AGTAAACATAGGTATAAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1300
SEQID14      AGTAAACATAGGTATAAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1246
SEQID18      AGTAAACATAGGTATAAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT 1156
SEQID13      -----

SEQID15      ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
SEQID17      ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1733
SEQID16      ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
SEQID12      ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1360
SEQID14      ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1306
SEQID18      ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA 1216
SEQID13      -----

SEQID15      ACTGGTAGCTATAAAGTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1366
SEQID17      ACTGGTAGCTATAAAGTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1793
SEQID16      ACTGGTAGCTATAAAGTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1366
SEQID12      ACTGGTAGCTATAAAGTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1420
SEQID14      ACTGGTAGCTATAAAGTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1366
SEQID18      ACTGGTAGCTATAAAGTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA 1276
SEQID13      -----

SEQID15      ATGAAATTTTCAATATTTGTTTCTTAT 1394
SEQID17      ATGAAATTTTCAATATTTGTTTCTTAT 1821
SEQID16      ATGAAATTTTCAATATTTGTTTCTTAT 1394
SEQID12      ATGAAATTTTCAATATTTGTTTCTTAT 1448
SEQID14      ATGAAATTTTCAATATTTGTTTCTTAT 1394
SEQID18      ATGAAATTTTCAATATTTGTTTCTTAT 1304
SEQID13      -----

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Fig 10.

SEQID19	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60
SEQID20	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60
SEQID21	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60

SEQID19	GGTTTTCTTCGTGTGTCTACAGGGCGCCCTGAGCCAGGTCCTGTTTGATGGCAGTTAT	120
SEQID20	GGTTTTCTTCGTGTGTCTACAGGGCGCCCTGAGCCAGGTCCTGTTTGATGGCAGTTAT	120
SEQID21	GGTTTTCTTCGTGTGTCTACAGGGCGCCCTGAGCCAGGTCCTGTTTGATGGCAGTTAT	120

SEQID19	GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCTGGCCTACTACTACTATTCTACAA	180
SEQID20	GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCTGGCCTACTACTACTATTCTACAA	180
SEQID21	GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCTGGCCTACTACTACTATTCTACAA	180

SEQID19	TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCA	240
SEQID20	TGAAGAGTTCAGAC-----	194
SEQID21	TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCA	240

SEQID19	AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAATGGGAGCCCATGTGGTATTGAC	300
SEQID20	-----	
SEQID21	AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAATGGGAGCCCATGTGGTATTGAC	300

SEQID19	TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC	360
SEQID20	-----TCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC	234
SEQID21	TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACTCGGAGCAGC	360

SEQID19	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTTATTGT	420
SEQID20	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTTATTGT	294
SEQID21	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTTATTGT	420

SEQID19	CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC	480
SEQID20	CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC	354
SEQID21	CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC	480

SEQID19	CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	540
SEQID20	CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	414
SEQID21	CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	540

SEQID19	CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	600
SEQID20	CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	474
SEQID21	CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	600

SEQID19	CATTGCCGTCACTCTCCTCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	660
SEQID20	CATTGCCGTCACTCTCCTCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	534
SEQID21	CATTGCCGTCACTCTCCTCTTGGCTGGGGGAA-GAACAGTTCACACAACAGAGA---AGTC	656

SEQID19	TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAAGCTCTACATAAC	720
SEQID20	TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAAGCTCTACATAAC	594
SEQID21	----GCAGTGTTACTCTGAC-----TCCCGC----GCCTGTGATTAATATCAC	698
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SEQID19	CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT	780
SEQID20	CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT	654
SEQID21	CAGCCACAGAATGGAC-TGGAACCTGTATC---GATCTGGTGGGATTGGATATAACGAA	754
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SEQID19	GAAGGAA--ATCTCTGGGATAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG	838
SEQID20	GAAGGAA--ATCTCTGGGATAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG	712
SEQID21	CATAGAATTACTCTCTGAGCTACCAAGCTGAA--TAGTTCAAATCAAATCATGCC--	808

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SEQID19	GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG	898					
SEQID20	GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG	772					
SEQID21	-AGAATATC--AGACAAATCCAAATGGCAAAAC-AGTTGCA-----	845					
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SEQID19	ACTCCAATCCTGCTTGCGGAACCCAGGAAGGAAGATCATGGAATTTTTTTCATTACGATAT	958					
SEQID20	ACTCCAATCCTGCTTGCGGAACCCAGGAAGGAAGATCATGGAATTTTTTTCATTACGATAT	832					
SEQID21	-----						
SEQID19	TATAATAAGGACATGTTTGTAAGTAACTAGGAACCTCTGAGCCCTGGTGAGTGGTCTTAG	1018					
SEQID20	TATAATAAGGACATGTTTGTAAGTAACTAGGAACCTCTGAGCCCTGGTGAGTGGTCTTAG	892					
SEQID21	-----						
SEQID19	AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA	1078					
SEQID16	AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA	952					
SEQID21	-----						
SEQID19	CAAATTTTGGGGTACACCTCATCATGAGAAATCTTGCAACACTTGCACAGTGAAATGT	1138					
SEQID20	CAAATTTTGGGGTACACCTCATCATGAGAAATCTTGCAACACTTGCACAGTGAAATGT	1012					
SEQID21	-----						
SEQID19	AATTGTAATAAATGTCAAAACCACTTTGGGGCCTGCAGTTGTGAACCTGATTGTAACATA	1198					
SEQID20	AATTGTAATAAATGTCAAAACCACTTTGGGGCCTGCAGTTGTGAACCTGATTGTAACATA	1072					
SEQID21	-----						
SEQID19	TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA	1258					
SEQID20	TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA	1132					
SEQID21	-----						
SEQID19	CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA	1307					
SEQID20	CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA	1181					
SEQID21	-----						